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SEQUENCE LISTING

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<120> PSEUDOTYPED RETROVIRUSES AND STABLE CELL LINES FOR THEIR PRODUCTION  
<130> 7024-497/PUR-115  
<140> US 09/762,224  
<141> 2001-02-02  
<150> PCT/US99/17702  
<151> 1999-08-04  
<150> U.S. 60/095,242  
<151> 1998-08-04  
<150> U.S. 60/112,405  
<151> 1998-12-15  
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tgc tca tca cct ccc tgc tac ccc tgc tgc tac gaa aaa cag cca gaa 96  
Cys Ser Ser Pro Pro Cys Tyr Pro Cys Cys Tyr Glu Lys Gln Pro Glu  
20 25 30

cag aca ctg cgg atg ctg gaa gac aat gtg aat aga cca ggg tac tat 144  
Gln Thr Leu Arg Met Leu Glu Asp Asn Val Asn Arg Pro Gly Tyr Tyr  
35 40 45

gag cta ctg gaa gcg tcc atg aca tgc aga aac aga tca cgc cac cgc Glu Leu Leu Glu Ala Ser Met Thr Cys Arg Asn Arg Ser Arg His Arg	192
50 55 60	
cgt agt gta aca gag cac ttc aat gtg tat aag gct act aga ccg tac Arg Ser Val Thr Glu His Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr	240
65 70 75 80	
tta gcg tat tgc gct gac tgt ggg gac ggg tac ttc tgc tat agc cca Leu Ala Tyr Cys Ala Asp Cys Gly Asp Gly Tyr Phe Cys Tyr Ser Pro	288
85 90 95	
gtt gct atc gag aag atc cga gat gag gcg tct gac ggc atg ctc aag Val Ala Ile Glu Lys Ile Arg Asp Glu Ala Ser Asp Gly Met Leu Lys	336
100 105 110	
atc caa gtc tcc gcc caa ata ggt ctg gac aag gca ggt acc cac gcc Ile Gln Val Ser Ala Gln Ile Gly Leu Asp Lys Ala Gly Thr His Ala	384
115 120 125	
cac acg aag atc cga tat atg gct ggt cat gat gtt cag gaa tct aag His Thr Lys Ile Arg Tyr Met Ala Gly His Asp Val Gln Glu Ser Lys	432
130 135 140	
aga gat tcc ttg agg gtg tac acg tcc gca gcg tgc tct ata cat ggg Arg Asp Ser Leu Arg Val Tyr Thr Ser Ala Ala Cys Ser Ile His Gly	480
145 150 155 160	
acg atg gga cac ttc atc gtc gca cat tgt ccg cca ggc gac tac ctc Thr Met Gly His Phe Ile Val Ala His Cys Pro Pro Gly Asp Tyr Leu	528
165 170 175	
aag gtt tcg ttc gag gac gca gat tca cac gtg aag gca tgt aag gtc Lys Val Ser Phe Glu Asp Ala Asp Ser His Val Lys Ala Cys Lys Val	576
180 185 190	
caa tac aag cac gac cca ttg ccg gtg ggt aga gag aag ttc gtg gtt Gln Tyr Lys His Asp Pro Leu Pro Val Gly Arg Glu Lys Phe Val Val	624
195 200 205	
aga ccc cac ttt ggc gta gag ctg cca tgc acc tca tac cag ctg aca Arg Pro His Phe Gly Val Glu Leu Pro Cys Thr Ser Tyr Gln Leu Thr	672
210 215 220	
aca gct ccc acc gac gag gag atc gac atg cac aca ccg cca gat ata Thr Ala Pro Thr Asp Glu Glu Ile Asp Met His Thr Pro Pro Asp Ile	720
225 230 235 240	
ccg gat cgc acc ctg cta tca cag acg gcg ggc aac gtc aaa ata aca Pro Asp Arg Thr Leu Leu Ser Gln Thr Ala Gly Asn Val Lys Ile Thr	768

	245	250	255	
gca ggc ggc agg act atc agg tac aat tgt acc tgt ggc cgt gac aac Ala Gly Gly Arg Thr Ile Arg Tyr Asn Cys Thr Cys Gly Arg Asp Asn	260	265	270	816
gta ggc act acc agt act gac aag acc atc aac aca tgc aag att gac Val Gly Thr Thr Ser Thr Asp Lys Thr Ile Asn Thr Cys Lys Ile Asp	275	280	285	864
caa tgc cat gct gcc gtt acc agc cat gac aaa tgg caa ttt acc tct Gln Cys His Ala Ala Val Thr Ser His Asp Lys Trp Gln Phe Thr Ser	290	295	300	912
cca ttt gtt ccc agg gct gat cag aca gct agg agg ggc aaa gtg cat Pro Phe Val Pro Arg Ala Asp Gln Thr Ala Arg Arg Gly Lys Val His	305	310	315	960
gtt cca ttc cct ttg act aac gtc acc tgc cga gtg ccg ttg gct cga Val Pro Phe Pro Leu Thr Asn Val Thr Cys Arg Val Pro Leu Ala Arg	325	330	335	1008
gcg ccg gat gtc acc tat ggt aag aag gag gtg acc ctg aga tta cac Ala Pro Asp Val Thr Tyr Gly Lys Lys Glu Val Thr Leu Arg Leu His	340	345	350	1056
cca gat cat ccg acg ctc ttc tcc tat agg agt tta gga gcc gaa ccg Pro Asp His Pro Thr Leu Phe Ser Tyr Arg Ser Leu Gly Ala Glu Pro	355	360	365	1104
cac ccg tac gag gag tgg gtt gac aag ttc tct gag cgc atc atc cca His Pro Tyr Glu Glu Trp Val Asp Lys Phe Ser Glu Arg Ile Ile Pro	370	375	380	1152
gtg acg gaa gaa ggg att gag tac cag tgg ggc aac aac ccg ccg gtc Val Thr Glu Glu Gly Ile Glu Tyr Gln Trp Gly Asn Asn Pro Pro Val	385	390	395	1200
cgc cta tgg gcg caa ctg acg acc gag ggc aaa ccc cat ggc tgg cca Arg Leu Trp Ala Gln Leu Thr Thr Glu Gly Lys Pro His Gly Trp Pro	405	410	415	1248
cat gaa atc att cag tac tat tat gga cta tac ccc gcc gcc acc att His Glu Ile Ile Gln Tyr Tyr Gly Leu Tyr Pro Ala Ala Thr Ile	420	425	430	1296
gcc gca gta tcc ggg gcg agt ctg atg gcc ctc cta act cta gcg gcc Ala Ala Val Ser Gly Ala Ser Leu Met Ala Leu Leu Thr Leu Ala Ala	435	440	445	1344
aca tgc tgc atg ctg gcc acc gcg agg aga aag tgc cta aca cca tac Thr Cys Cys Met Leu Ala Thr Ala Arg Arg Lys Cys Leu Thr Pro Tyr	450	455	460	1392
gcc ttg acg cca gga gcg gtg gta ccg ttg aca ctg ggg ctg ctt tgc Ala Leu Thr Pro Gly Ala Val Val Pro Leu Thr Leu Gly Leu Leu Cys	465	470	475	1440

tgc gca ccg agg gcg aac gca gca tca ttc gct gag act atg gca tat Cys Ala Pro Arg Ala Asn Ala Ala Ser Phe Ala Glu Thr Met Ala Tyr 485 490 495	1488
ctg tgg gac gag aac aaa acc ctc ttt tgg atg gaa ttc gcc gcc cca Leu Trp Asp Glu Asn Lys Thr Leu Phe Trp Met Glu Phe Ala Ala Pro 500 505 510	1536
gcc gca gcg ctt gct ttg ctg gca tgc tgt atc aaa agc ctg atc tgc Ala Ala Ala Leu Ala Leu Ala Cys Cys Ile Lys Ser Leu Ile Cys 515 520 525	1584
tgt tgt aag cca ttt tct ttt tta gtg tta ctg agc ctg gga gcc tcc Cys Cys Lys Pro Phe Ser Phe Leu Val Leu Ser Leu Gly Ala Ser 530 535 540	1632
gca aaa gct tac gag cac aca gca att ccg aat gtg gtg ggg ttc Ala Lys Ala Tyr Glu His Thr Ala Thr Ile Pro Asn Val Val Gly Phe 545 550 555 560	1680
ccg tat aag gct cac att gaa agg aat ggc ttc tcg ccc atg act ctg Pro Tyr Lys Ala His Ile Glu Arg Asn Gly Phe Ser Pro Met Thr Leu 565 570 575	1728
cag ctt gaa gtg gtg gag aca agc ttg gaa ccc aca ctt aac ctg gag Gln Leu Glu Val Val Glu Thr Ser Leu Glu Pro Thr Leu Asn Leu Glu 580 585 590	1776
tac att acc tgc gaa tac aag acg gtg gtc cct tcg cca ttc atc aaa Tyr Ile Thr Cys Glu Tyr Lys Thr Val Val Pro Ser Pro Phe Ile Lys 595 600 605	1824
tgt tgc gga aca tca gaa tgc tca tcc aag gag cag cca gac tac caa Cys Cys Gly Thr Ser Glu Cys Ser Ser Lys Glu Gln Pro Asp Tyr Gln 610 615 620	1872
tgc aag gtg tac acg ggt gta tac cca ttc atg tgg ggt gga gcc tac Cys Lys Val Tyr Thr Gly Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr 625 630 635 640	1920
tgt ttc tgc gac tcc gag aac acg cag ctc agc gag gcc tat gtc gac Cys Phe Cys Asp Ser Glu Asn Thr Gln Leu Ser Glu Ala Tyr Val Asp 645 650 655	1968
agg tca gac gtt tgc aaa cat gat cac gca tcg gcc tac aag gca cac Arg Ser Asp Val Cys Lys His Asp His Ala Ser Ala Tyr Lys Ala His 660 665 670	2016
acg gcc tct cta aaa gca aca atc agg atc agt tat ggc acc atc aac Thr Ala Ser Leu Lys Ala Thr Ile Arg Ile Ser Tyr Gly Thr Ile Asn 675 680 685	2064
cag acc acc gag gcc ttc gtt aat ggt gaa cac gca gtc aac gtg ggc Gln Thr Thr Glu Ala Phe Val Asn Gly Glu His Ala Val Asn Val Gly 690 695 700	2112

gga agc aag ttc atc ttt gga ccg atc tca aca gct tgg tca ccg ttc Gly Ser Lys Phe Ile Phe Gly Pro Ile Ser Thr Ala Trp Ser Pro Phe	705	710	715	720	2160
gac aat aaa att gtc gtg tat aaa gat gat gtc tac aac cag gac ttc Asp Asn Lys Ile Val Val Tyr Lys Asp Asp Val Tyr Asn Gln Asp Phe	725	730	735		2208
cca ccc tac gga tca ggc cag ccg ggt aga ttc gga gac att cag agc Pro Pro Tyr Gly Ser Gly Gln Pro Gly Arg Phe Gly Asp Ile Gln Ser	740	745	750		2256
agg aca gtg gag agc aaa gac ttg tat gcc aac acg gcc cta aaa ctc Arg Thr Val Glu Ser Lys Asp Leu Tyr Ala Asn Thr Ala Leu Lys Leu	755	760	765		2304
tca aga cca tca ccc ggg gtt gtg cat gtg cca tac acg cag aca cca Ser Arg Pro Ser Pro Gly Val Val His Val Pro Tyr Thr Gln Thr Pro	770	775	780		2352
tcc gga ttt aaa tat tgg ctg aag gag aaa gga tct tca ttg aat aca Ser Gly Phe Lys Tyr Trp Leu Lys Glu Lys Gly Ser Ser Leu Asn Thr	785	790	795	800	2400
aag gcc cct ttt ggc tgc aag ata aag acc aat cca gtc aga gcc atg Lys Ala Pro Phe Gly Cys Ile Lys Thr Asn Pro Val Arg Ala Met	805	810	815		2448
gat tgt gca gtt ggc agt ata cct gtg tcg atg gac ata cct gac agt Asp Cys Ala Val Gly Ser Ile Pro Val Ser Met Asp Ile Pro Asp Ser	820	825	830		2496
gca ttc aca cga gtg gta gat gcc ccg gct gta aca gac ctg agc tgc Ala Phe Thr Arg Val Val Asp Ala Pro Ala Val Thr Asp Leu Ser Cys	835	840	845		2544
cag gta gtg gtc tgt aca cac tcc tcc gat ttc gga gga gtt gcc aca Gln Val Val Val Cys Thr His Ser Ser Asp Phe Gly Gly Val Ala Thr	850	855	860		2592
ttg tct tac aaa acg gac aaa ccc ggc aag tgc gct gtc cac tca cat Leu Ser Tyr Lys Thr Asp Lys Pro Gly Lys Cys Ala Val His Ser His	865	870	875	880	2640
tcc aac gtc gca acg ttg caa gag gcg acg gtg gat gtc aag gag gat Ser Asn Val Ala Thr Leu Gln Glu Ala Thr Val Asp Val Lys Glu Asp	885	890	895		2688
ggc aag gtc aca gtg cac ttt tcc acg gcg tcc gcc tcc ccg gcc ttc Gly Lys Val Thr Val His Phe Ser Thr Ala Ser Ala Ser Pro Ala Phe	900	905	910		2736
aaa gtg tcc gtc tgt gac gca aaa aca acg tgc acg gcg gcg tgc gag Lys Val Ser Val Cys Asp Ala Lys Thr Thr Cys Thr Ala Ala Cys Glu	915	920	925		2784
cct cca aaa gac cac atc gtc cct tat ggg gcg agc cat aac aac cag					2832

Pro Pro Lys Asp His Ile Val Pro Tyr Gly Ala Ser His Asn Asn Gln  
 930 935 940

gtc ttt ccg gac atg tca gga act gcg atg acg tgg gtg cag agg ctg 2880  
 Val Phe Pro Asp Met Ser Gly Thr Ala Met Thr Trp Val Gln Arg Leu  
 945 950 955 960

gcc agt ggg tta ggt ggg ctg gct ctc atc gcg gtg gtt gtg ctg gtc 2928  
 Ala Ser Gly Leu Gly Leu Ala Leu Ile Ala Val Val Val Leu Val  
 965 970 975

ttg gta acc tgc ata aca atg cgt cggt taa 2958  
 Leu Val Thr Cys Ile Thr Met Arg Arg  
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<211> 2176

<212> DNA

<213> Filovirus Ebola virus, subtype Zaire

<400> 2

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 1 5 10 15

agg aca tca ttc ttt ctt tgg gta att atc ctt ttc caa aga aca ttt 103  
 Arg Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe  
 20 25 30

tcc atc cca ctt gga gtc atc cac aat agc aca tta cag gtt agt gat 151  
 Ser Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp  
 35 40 45

gtc gac aaa cta gtt tgt cgt gac aaa ctg tca tcc aca aat caa ttg 199  
 Val Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu  
 50 55 60

aga tca gtt gga ctg aat ctc gaa ggg aat gga gtg gca act gac gtg 247  
 Arg Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val  
 65 70 75

cca tct gca act aaa aga tgg ggc ttc agg tcc ggt gtc cca cca aag 295  
 Pro Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys  
 80 85 90 95

gtg gtc aat tat gaa gct ggt gaa tgg gct gaa aac tgc tac aat ctt 343  
 Val Val Asn Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu  
 100 105 110

gaa atc aaa aaa cct gac ggg agt gag tgt cta cca gca gcg cca gac 391  
 Glu Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Ala Ala Pro Asp  
 115 120 125

ggg att cg <sup>g</sup> ggc ttc ccc cgg tgc cg <sup>g</sup> tat gtg cac aaa gta tca gg <sup>a</sup>	130	135	140	439
Gly Ile Arg Gly Phe Pro Arg Cys Arg Tyr Val His Lys Val Ser Gly				
acg gga ccg tgt gcc gga gac ttt gcc ttc cat aaa gag ggt gct ttc	145	150	155	487
Thr Gly Pro Cys Ala Gly Asp Phe Ala Phe His Lys Glu Gly Ala Phe				
ttc ctg tat gat cga ctt gct tcc aca gtt atc tac cga gga acg act	160	165	170	535
Phe Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Thr Thr				
ttc gct gaa ggt gtc gtt gca ttt ctg ata ctg ccc caa gct aag aag	180	185	190	583
Phe Ala Glu Gly Val Val Ala Phe Leu Ile Leu Pro Gln Ala Lys Lys				
gac ttc ttc agc tca cac ccc ttg aga gag ccg gtc aat gca acg gag	195	200	205	631
Asp Phe Phe Ser Ser His Pro Leu Arg Glu Pro Val Asn Ala Thr Glu				
gac ccg tct agt ggc tac tat tct acc aca att aga tat cag gct acc	210	215	220	679
Asp Pro Ser Ser Gly Tyr Tyr Ser Thr Thr Ile Arg Tyr Gln Ala Thr				
ggt ttt gga acc aat gag aca gag tac ttg ttc gag gtt gac aat ttg	225	230	235	727
Gly Phe Gly Thr Asn Glu Thr Glu Tyr Leu Phe Glu Val Asp Asn Leu				
acc tac gtc caa ctt gaa tca aga ttc aca cca cag ttt ctg ctc cag	240	245	250	757
Thr Tyr Val Gln Leu Glu Ser Arg Phe Thr Pro Gln Phe Leu Leu Gln				
ctg aat gag aca ata tat aca agt ggg aaa agg agc aat acc acg gga	260	265	270	775
Leu Asn Glu Thr Ile Tyr Thr Ser Gly Lys Arg Ser Asn Thr Thr Gly				
aaa cta att tgg aag gtc aac ccc gaa att gat aca aca atc ggg gag	275	280	285	823
Lys Leu Ile Trp Lys Val Asn Pro Glu Ile Asp Thr Thr Ile Gly Glu				
tgg gcc ttc tgg gaa act aaa aaa aAc ctc act aga aaa att cgc agt	290	295	300	871
Trp Ala Phe Trp Glu Thr Lys Lys Asn Leu Thr Arg Lys Ile Arg Ser				
gaa gag ttg tct ttc aca gtt gta tca aac gga gcc aaa aac atc agt	305	310	315	919
Glu Glu Leu Ser Phe Thr Val Val Ser Asn Gly Ala Lys Asn Ile Ser				
ggt cag agt ccg gcg cga act tct tcc gac cca ggg acc aac aca aca	320	325	330	967
Gly Gln Ser Pro Ala Arg Thr Ser Ser Asp Pro Gly Thr Asn Thr Thr				
act gaa gac cac aaa atc atg gct tca gaa aat tcc tct gca atg gtt	340	345	350	1015
Thr Glu Asp His Lys Ile Met Ala Ser Glu Asn Ser Ser Ala Met Val				

caa gtg cac agt caa gga agg gaa gct gca gtg tcg cat cta aca acc Gln Val His Ser Gln Gly Arg Glu Ala Ala Val Ser His Leu Thr Thr 355 360 365	1063
ctt gcc aca atc tcc acg agt ccc caa tcc ctc aca acc aaa cca ggt Leu Ala Thr Ile Ser Thr Ser Pro Gln Ser Leu Thr Thr Lys Pro Gly 370 375 380	1111
ccg gac aac agc acc cat aat aca ccc gtg tat aaa ctt gac atc tct Pro Asp Asn Ser Thr His Asn Thr Pro Val Tyr Lys Leu Asp Ile Ser 385 390 395	1159
gag gca act caa gtt gaa caa cat cac cgc aga aca gac aac gac agc Glu Ala Thr Gln Val Glu Gln His His Arg Arg Thr Asp Asn Asp Ser 400 405 410 415	1207
aca gcc tcc gac act ccc tct gcc acg acc gca gcc gga ccc cca aaa Thr Ala Ser Asp Thr Pro Ser Ala Thr Ala Ala Gly Pro Pro Lys 420 425 430	1255
gca gag aac acc aac acg agc aag agc act gac ttc ctg gac ccc gcc Ala Glu Asn Thr Asn Thr Ser Lys Ser Thr Asp Phe Leu Asp Pro Ala 435 440 445	1303
acc aca aca agt ccc caa aac cac agc gag acc gct ggc aac aac aac Thr Thr Ser Pro Gln Asn His Ser Glu Thr Ala Gly Asn Asn Asn 450 455 460	1351
act cat cac caa gat acc gga gaa gag agt gcc agc agc ggg aag cta Thr His His Gln Asp Thr Gly Glu Glu Ser Ala Ser Ser Gly Lys Leu 465 470 475	1399
ggc tta att acc aat act att gct gga gtc gca gga ctg atc aca ggc Gly Leu Ile Thr Asn Thr Ile Ala Gly Val Ala Gly Leu Ile Thr Gly 485 490 495 500	1447
ggg aga aga act cga aga gaa gca att gtc aat gct caa ccc aaa tgc Gly Arg Arg Thr Arg Arg Glu Ala Ile Val Asn Ala Gln Pro Lys Cys 505 510 515	1495
aac cct aat tta cat tac tgg act act cag gat gaa ggt gct gca atc Asn Pro Asn Leu His Tyr Trp Thr Thr Gln Asp Glu Gly Ala Ala Ile 520 525 530	1543
gga ctg gcc tgg ata cca tat ttc ggg cca gca gcc gag gga att tac Gly Leu Ala Trp Ile Pro Tyr Phe Gly Pro Ala Ala Glu Gly Ile Tyr 535 540 545	1591
ata gag ggg cta atg cac aat caa gat ggt tta atc tgt ggg ttg aga Ile Glu Gly Leu Met His Asn Gln Asp Gly Leu Ile Cys Gly Leu Arg 550 555 560	1639
cag ctg gcc aac gag acg act caa gct ctt caa ctg ttc ctg aga gcc Gln Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu Arg Ala 565 570 575 580	1687
aca act gag cta cgc acc ttt tca atc ctc aac cgt aag gca att gat	1735

Thr Thr Glu Leu Arg Thr Phe Ser Ile Leu Asn Arg Lys Ala Ile Asp			
585	590	595	
ttc ttg ctg cag cga tgg ggc ggc aca tgc cac att ctg gga ccg gac			1783
Phe Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly Pro Asp			
600	605	610	
tgc tgt atc gaa cca cat gat tgg acc aag aac ata aca gac aaa att			1831
Cys Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile			
615	620	625	
gat cag att att cat gat ttt gtt gat aaa acc ctt ccg gac cag ggg			1879
Asp Gln Ile Ile His Asp Phe Val Asp Lys Thr Leu Pro Asp Gln Gly			
630	635	640	
gac aat gac aat tgg tgg aca gga tgg aga caa tgg ata ccg gca ggt			1927
Asp Asn Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro Ala Gly			
645	650	655	660
att gga gtt aca ggc gtt ata att gca gtt atc gct tta ttc tgt ata			1975
Ile Gly Val Thr Gly Val Ile Ile Ala Val Ile Ala Leu Phe Cys Ile			
665	670	675	
tgc aaa ttt gtc ttt tag tttttcttca gattgcttca tggaaaaagct cagcctcaaa			2033
Cys Lys Phe Val Phe			
680			
tcaatgaaac caggatttaa ttatatggat tacttgaatc taagattact tgacaaatga			2093
taatataata cactggagct ttaaacatag ccaatgtgat tctaactcct ttaaactcac			2153
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Met lys thr thr cys phe leu ile ser leu ile leu ile gln gly			
1	5	10	15
aca aaa aat ctc ccc att tta gag ata gct agt aat aat caa ccc caa			102
thr lys asn leu pro ile leu glu ile ala ser asn asn gln pro gln			
20	25	30	
aat gtg gat tcg gta tgc tcc gga act ctc cag aag aca gaa gac gtc			150
asn val asp ser val cys ser gly thr leu gln lys thr glu asp val			
35	40	45	

cat ctg atg gga ttc aca ctg agt ggg caa aaa gtt gct gat tcc cct his leu met gly phe thr leu ser gly gln lys val ala asp ser pro	50	55	60	198	
ttg gag gca tcc aag cga tgg gct ttc agg aca ggt gta cct ccc aag leu glu ala ser lys arg trp ala phe arg thr gly val pro pro lys	65	70	75	246	
aat gtt gag tac aca gag ggg gag gaa gcc aaa aca tgc tac aat ata asn val glu tyr thr glu gly glu ala lys thr cys tyr asn ile	80	85	90	294	
agt gta acg gat ccc tct gga aaa tcc ttg ctg tta gat cct cct acc ser val thr asp pro ser gly lys ser leu leu leu asp pro pro thr	100	105	110	342	
aac atc cgt gac tat cct aaa tgc aaa act atc cat cat att caa ggt asn ile arg asp tyr pro lys cys lys thr ile his his ile gln gly	115	120	125	390	
caa aac cct cat gca cag ggg atc gcc ctt cat tta tgg gga gca ttt gln asn pro his ala gln gly ile ala leu his leu trp gly ala phe	130	135	140	438	
ttt ctg tat gat cgc att gcc tcc aca aca atg tac cga ggc aaa gtc phe leu tyr asp arg ile ala ser thr thr met tyr arg gly lys val	145	150	155	486	
ttc act gaa ggg aac ata gca gct atg att gtc aat aag aca gtg cac phe thr glu gly asn ile ala ala met ile val asn lys thr val his	160	165	170	175	534
aaa atg att ttc tcg cgg caa gga caa ggg tac cgt cat atg aat ctg lys met ile phe ser arg gln gly gln gly tyr arg his met asn leu	180	185	190	582	
act tct act aat aaa tat tgg aca agt agt aac gga acg caa acg aat thr ser thr asn lys tyr trp thr ser ser asn gly thr gln thr asn	195	200	205	630	
gac act gga tgt ttc ggc gct ctt caa gaa tac aat tct aca aag aac asp thr gly cys phe gly ala leu gln glu tyr asn ser thr lys asn	210	215	220	678	
caa aca tgt gct ccg tcc aaa ata cct cca cca ctg ccc aca gcc cgt gln thr cys ala pro ser lys ile pro pro pro leu pro thr ala arg	225	230	235	240	726
ccg gag atc aaa ctc aca agc acc cca act gat gcc acc aaa ctc aat pro glu ile lys leu thr ser thr pro thr asp ala thr lys leu asn	245	250	255	774	
acc acg gac cca agc agt gat gat gag gac ctc gca aca tcc ggc tca thr thr asp pro ser ser asp asp glu asp leu ala thr ser gly ser	260	265	270	822	
ggg tcc gga gaa cga gaa ccc cac aca act tct gat gcg gtc acc aag				870	

gly ser gly glu arg glu pro his thr thr ser asp ala val thr lys			
275	280	285	
caa ggg ctt tca tca aca atg cca ccc act ccc tca cca caa cca agc			918
gln gly leu ser ser thr met pro pro thr pro ser pro gln pro ser			
290	295	300	
acg cca cag caa gga gga aac aac aca aac cat tcc caa gat gct gtg			966
thr pro gln gln gly gly asn asn thr asn his ser gln asp ala val			
305	310	315	320
act gaa cta gac aaa aat aac aca act gca caa ccg tcc atg ccc cct			1014
thr glu leu asp lys asn asn thr thr ala gln pro ser met pro pro			
325	330	335	
cat aac act acc aca atc tct act aac aac acc tcc aaa cac aac ttc			1062
his asn thr thr thr ile ser thr asn asn thr ser lys his asn phe			
340	345	350	
agc act ctc tct gca cca tta caa aac acc acc acc aat gac aac aca cag			1110
ser thr leu ser ala pro leu gln asn thr thr asn asp asn thr gln			
355	360	365	
agc aca atc act gaa aat gag caa acc agt gcc ccc tcg ata aca acc			1158
ser thr ile thr glu asn glu gln thr ser ala pro ser ile thr thr			
370	375	380	
ctg cct cca acg gga aat ccc acc aca gca aag agc acc agc agc aaa			1206
leu pro pro thr gly asn pro thr thr ala lys ser thr ser ser lys			
385	390	395	400
aaa ggc ccc gcc aca acg gca cca aac acg aca aat gag cat ttc acc			1254
lys gly pro ala thr thr ala pro asn thr thr asn glu his phe thr			
405	410	415	
agt cct ccc ccc acc ccc agc tcg act gca caa cat ctt gta tat ttc			1302
ser pro pro pro thr pro ser ser thr ala gln his leu val tyr phe			
420	425	430	
aga aga aag cga agt atc ctc tgg agg gaa ggc gac atg ttc cct ttt			1350
arg arg lys arg ser ile leu trp arg glu gly asp met phe pro phe			
435	440	445	
ctg gat ggg tta ata aat gct cca att gat ttt gac cca gtt cca aat			1398
leu asp gly leu ile asn ala pro ile asp phe asp pro val pro asn			
450	455	460	
aca aaa aca atc ttt gat gaa tcc tct agt tct ggt gcc tcg gct gag			1446
thr lys thr ile phe asp glu ser ser ser gly ala ser ala glu			
465	470	475	480
gaa gat caa cat gcc tcc ccc aat att agt tta act tta tct tat ttt			1494
glu asp gln his ala ser pro asn ile ser leu thr leu ser tyr phe			
485	490	495	
cct aat ata aat gag aac act gcc tac tct gga gaa aat gag aat gat			1542
pro asn ile asn glu asn thr ala tyr ser gly glu asn glu asp			

500	505	510	
tgt gat gca gag tta aga att tgg agc gtt cag gag gat gac ctg gcc cys asp ala glu leu arg ile trp ser val gln glu asp asp leu ala 515	520	525	1590
gca ggg ctc agt tgg ata ccg ttt ttt ggc cct gga att gaa gga ctt ala gly leu ser trp ile pro phe phe gly pro gly ile glu gly leu 530	535	540	1638
tac act gct gtt tta att aaa aat caa aac aat ttg gtc tgc agg ttg tyr thr ala val leu ile lys asn gln asn asn leu val cys arg leu 545	550	555	1686
agg cgt cta gcc aat caa act gcc aaa tcc ttg gaa ctc tta ttg aga arg arg leu ala asn gln thr ala lys ser leu glu leu leu arg 565	570	575	1734
gtc aca act gag gaa aga aca ttc tcc tta atc aat aga cat gct att val thr thr glu glu arg thr phe ser leu ile asn arg his ala ile 580	585	590	1782
gac ttt cta ctc aca aga tgg gga gga aca tgc aaa gtg ctt gga cct asp phe leu leu thr arg trp gly gly thr cys lys val leu gly pro 595	600	605	1830
gat tgt tgc atc ggg ata gaa gac ttg tcc aaa aat att tca gag caa asp cys cys ile gly ile glu asp leu ser lys asn ile ser glu gln 610	615	620	1878
att gac caa att aaa aag gac gaa caa aaa gag ggg act ggt tgg ggt ile asp gln ile lys lys asp glu gln lys glu gly thr trp gly 625	630	635	1926
ctg ggt aaa tgg tgg aca tcc gac tgg ggt gtt ctt act aac ttg leu gly gly lys trp trp thr ser asp trp gly val leu thr asn leu 645	650	655	1974
ggc att ttg cta cta tta tcc ata gct gtc ttg att gct cta tcc tgt gly ile leu leu leu leu ser ile ala val leu ile ala leu ser cys 660	665	670	2022
att tgt cgt atc ttt act aaa tat atc gga taa cgtta aatgtgtaat gattaggact ile cys arg ile phe thr lys tyr ile gly 675	680		2080
ttaggacaat tgctactgag ccc			2103